1600

RAW SEQUENCE LISTING
PATENT APPLICATION: **US/09/468,002**

DATE: 03/31/2003
TIME: 16:26:36

Input Set : **N:\Crf3\RULE60\09468002.raw**
Output Set: **N:\CRF4\03312003\I468002.raw**

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 1 <110> APPLICANT: Negulescu, Paul
 2        Offermanns, Stefan
 3        Simon, Melvin
 4        Zuker, Charles
 5 <120> TITLE OF INVENTION: PROMISCUOUS G-PROTEINS COMPOSITIONS AND THEIR USE
 6 <130> FILE REFERENCE: 08366/002001
 7 <140> CURRENT APPLICATION NUMBER: 09/468,002
 8 <141> CURRENT FILING DATE: 1999-12-20
 9 <150> PRIOR APPLICATION NUMBER: US/08/878,801
10 <151> PRIOR FILING DATE: 1997-06-19
11 <150> PRIOR APPLICATION NUMBER: US 60/020,234
12 <151> PRIOR FILING DATE: 1996-06-21
13 <160> NUMBER OF SEQ ID NOS: 4
14 <170> SOFTWARE: FastSEQ for Windows Version 3.0
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17 <211> LENGTH: 1125
18 <212> TYPE: DNA
19 <213> ORGANISM: Mus musculus
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21 <221> NAME/KEY: CDS
22 <222> LOCATION: (1)...(1122)
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25       Met Ala Arg Ser Leu Thr Trp Arg Cys Cys Pro Trp Cys Leu Thr Glu
26        1               5                  10                  15
27       gat gag aag gcc gcc gcc cgg gtg gac cag gag atc aac agg atc ctc      96
28       Asp Glu Lys Ala Ala Ala Arg Val Asp Gln Glu Ile Asn Arg Ile Leu
29                      20                  25                  30
30       ttg gag cag aag aag cag gac cgc ggg gag ctg aag ctg ctg ctt ttg     144
31       Leu Glu Gln Lys Lys Gln Asp Arg Gly Glu Leu Lys Leu Leu Leu Leu
32                  35                  40                  45
33       ggc cca ggc gag agc ggg aag agc acc ttc atc aag cag atg cgg atc     192
34       Gly Pro Gly Glu Ser Gly Lys Ser Thr Phe Ile Lys Gln Met Arg Ile
35         ·  50                  55                  60
36       atc cac ggc gcc ggc tac tcg gag gag gag cgc aag ggc ttc cgg ccc     240
37       Ile His Gly Ala Gly Tyr Ser Glu Glu Glu Arg Lys Gly Phe Arg Pro
38         65                  70                  75                  80
39       ctg gtc tac cag aac atc ttc gtg tcc atg cgg gcc atg atc gag gcc     288
40       Leu Val Tyr Gln Asn Ile Phe Val Ser Met Arg Ala Met Ile Glu Ala
41                          85                  90                  95
42       atg gag cgg ctg cag att cca ttc agc agg ccc gag agc aag cac cac     336
43       Met Glu Arg Leu Gln Ile Pro Phe Ser Arg Pro Glu Ser Lys His His
44                         100                 105                 110
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45      gct agc ctg gtc atg agc cag gac ccc tat aaa gtg acc acg ttt gag      384
46      Ala Ser Leu Val Met Ser Gln Asp Pro Tyr Lys Val Thr Thr Phe Glu
47              115                 120                 125
48      aag cgc tac gct gcg gcc atg cag tgg ctg tgg agg gat gcc ggc atc      432
49      Lys Arg Tyr Ala Ala Ala Met Gln Trp Leu Trp Arg Asp Ala Gly Ile
50              130                 135                 140
51      cgg gcc tgc tat gag cgt cgg cgg gaa ttc cac ctg ctc gat tca gcc      480
52      Arg Ala Cys Tyr Glu Arg Arg Arg Glu Phe His Leu Leu Asp Ser Ala
53      145                 150                 155                 160
54      gtg tac tac ctg tcc cac ctg gag cgc atc acc gag gag ggc tac gtc      528
55      Val Tyr Tyr Leu Ser His Leu Glu Arg Ile Thr Glu Glu Gly Tyr Val
56                          165                 170                 175
57      ccc aca gct cag gac gtg ctc cgc agc cgc atg ccc acc act ggc atc      576
58      Pro Thr Ala Gln Asp Val Leu Arg Ser Arg Met Pro Thr Thr Gly Ile
59                  180                 185                 190
60      aac gag tac tgc ttc tcc gtg cag aaa acc aac ctg cgg atc gtg gac      624
61      Asn Glu Tyr Cys Phe Ser Val Gln Lys Thr Asn Leu Arg Ile Val Asp
62              195                 200                 205
63      gtc ggg ggc cag aag tca gag cgt aag aaa tgg atc cat tgt ttc gag      672
64      Val Gly Gly Gln Lys Ser Glu Arg Lys Lys Trp Ile His Cys Phe Glu
65              210                 215                 220
66      aac gtg atc gcc ctc atc tac ctg gcc tca ctg agt gaa tac gac cag      720
67      Asn Val Ile Ala Leu Ile Tyr Leu Ala Ser Leu Ser Glu Tyr Asp Gln
68      225                 230                 235                 240
69      tgc ctg gag gag aac aac cag gag aac cgc atg aag gag agc ctc gca      768
70      Cys Leu Glu Glu Asn Asn Gln Glu Asn Arg Met Lys Glu Ser Leu Ala
71                          245                 250                 255
72      ttg ttt ggg act atc ctg gaa cta ccc tgg ttc aaa agc aca tcc gtc      816
73      Leu Phe Gly Thr Ile Leu Glu Leu Pro Trp Phe Lys Ser Thr Ser Val
74                  260                 265                 270
75      atc ctc ttt ctc aac aaa acc gac atc ctg gag gag aaa atc ccc acc      864
76      Ile Leu Phe Leu Asn Lys Thr Asp Ile Leu Glu Glu Lys Ile Pro Thr
77              275                 280                 285
78      tcc cac ctg gct acc tat ttc ccc agt ttc cag ggc cct aag cag gat      912
79      Ser His Leu Ala Thr Tyr Phe Pro Ser Phe Gln Gly Pro Lys Gln Asp
80              290                 295                 300
81      gct gag gca gcc aag agg ttc atc ctg gac atg tac acg agg atg tac      960
82      Ala Glu Ala Ala Lys Arg Phe Ile Leu Asp Met Tyr Thr Arg Met Tyr
83      305                 310                 315                 320
84      acc ggg tgc gtg gac ggc ccc gag ggc agc aag aag ggc gca cga tcc      1008
85      Thr Gly Cys Val Asp Gly Pro Glu Gly Ser Lys Lys Gly Ala Arg Ser
86                          325                 330                 335
87      cga cgc ctt ttc agc cac tac aca tgt gcc aca gac aca cag aac atc      1056
88      Arg Arg Leu Phe Ser His Tyr Thr Cys Ala Thr Asp Thr Gln Asn Ile
89                  340                 345                 350
90      cgc aag gtc ttc aag gac gtg cgg gac tcg gtg ctc gcc cgc tac ctg      1104
91      Arg Lys Val Phe Lys Asp Val Arg Asp Ser Val Leu Ala Arg Tyr Leu
92                  355                 360                 365
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98 <211> LENGTH: 374
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105                     20                  25                  30
106         Leu Glu Gln Lys Lys Gln Asp Arg Gly Glu Leu Lys Leu Leu Leu Leu
107                 35                  40                  45
108         Gly Pro Gly Glu Ser Gly Lys Ser Thr Phe Ile Lys Gln Met Arg Ile
109             50                  55                  60
110         Ile His Gly Ala Gly Tyr Ser Glu Glu Glu Arg Lys Gly Phe Arg Pro
111             65                  70                  75                  80
112         Leu Val Tyr Gln Asn Ile Phe Val Ser Met Arg Ala Met Ile Glu Ala
113                         85                  90                  95
114         Met Glu Arg Leu Gln Ile Pro Phe Ser Arg Pro Glu Ser Lys His His
115                     100                 105                 110
116         Ala Ser Leu Val Met Ser Gln Asp Pro Tyr Lys Val Thr Thr Phe Glu
117                 115                 120                 125
118         Lys Arg Tyr Ala Ala Ala Met Gln Trp Leu Trp Arg Asp Ala Gly.Ile
119             130                 135                 140
120         Arg Ala Cys Tyr Glu Arg Arg Arg Glu Phe His Leu Leu Asp Ser Ala
121         145                 150                 155                 160
122         Val Tyr Tyr Leu Ser His Leu Glu Arg Ile Thr Glu Glu Gly Tyr Val
123                         165                 170                 175
124         Pro Thr Ala Gln Asp Val Leu Arg Ser Arg Met Pro Thr Thr Gly Ile
125                     180                 185                 190
126         Asn Glu Tyr Cys Phe Ser Val Gln Lys Thr Asn Leu Arg Ile Val Asp
127                 195                 200                 205
128         Val Gly Gly Gln Lys Ser Glu Arg Lys Lys Trp Ile His Cys Phe Glu
129             210                 215                 220
130         Asn Val Ile Ala Leu Ile Tyr Leu Ala Ser Leu Ser Glu Tyr Asp Gln
131         225                 230                 235                 240
132         Cys Leu Glu Glu Asn Asn Gln Glu Asn Arg Met Lys Glu Ser Leu Ala
133                     245                 250                 255
134         Leu Phe Gly Thr Ile Leu Glu Leu Pro Trp Phe Lys Ser Thr Ser Val
135                 260                 265                 270
136         Ile Leu Phe Leu Asn Lys Thr Asp Ile Leu Glu Glu Lys Ile Pro Thr
137                 275                 280                 285
138         Ser His Leu Ala Thr Tyr Phe Pro Ser Phe Gln Gly Pro Lys Gln Asp
139             290                 295                 300
140         Ala Glu Ala Ala Lys Arg Phe Ile Leu Asp Met Tyr Thr Arg Met Tyr
141         305                 310                 315                 320
142         Thr Gly Cys Val Asp Gly Pro Glu Gly Ser Lys Lys Gly Ala Arg Ser
143                     325                 330                 335
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144        Arg Arg Leu Phe Ser His Tyr Thr Cys Ala Thr Asp Thr Gln Asn Ile
145                    340                 345                 350
146        Arg Lys Val Phe Lys Asp Val Arg Asp Ser Val Leu Ala Arg Tyr Leu
147                    355                 360                 365
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153  <212> TYPE: DNA
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156  <221> NAME/KEY: CDS
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160        Met Ala Arg Ser Leu Thr Trp Gly Cys Cys Pro Trp Cys Leu Thr Glu
161         1               5                  10                  15
162        gag gag aag act gcc gcc aga atc gac cag gag atc aac agg att ttg    96
163        Glu Glu Lys Thr Ala Ala Arg Ile Asp Gln Glu Ile Asn Arg Ile Leu
164                     20                  25                  30
165        ttg gaa cag aaa aaa caa gag cgc gag gaa ttg aaa ctc ctg ctg ttg   144
166        Leu Glu Gln Lys Lys Gln Glu Arg Glu Glu Leu Lys Leu Leu Leu Leu
167                     35                  40                  45
168        ggg cct ggt gag agc ggg aag agt acg ttc atc aag cag atg cgc atc   192
169        Gly Pro Gly Glu Ser Gly Lys Ser Thr Phe Ile Lys Gln Met Arg Ile
170                     50                  55                  60
171        att cac ggt gtg ggc tac tcg gag gag gac cgc aga gcc ttc cgg ctg   240
172        Ile His Gly Val Gly Tyr Ser Glu Glu Asp Arg Arg Ala Phe Arg Leu
173         65                  70                  75                  80
174        ctc atc tac cag aac atc ttc gtc tcc atg cag gcc atg ata gat gcg   288
175        Leu Ile Tyr Gln Asn Ile Phe Val Ser Met Gln Ala Met Ile Asp Ala
176                             85                  90                  95
177        atg gac cgg ctg cag atc ccc ttc agc agg cct gac agc aag cag cac   336
178        Met Asp Arg Leu Gln Ile Pro Phe Ser Arg Pro Asp Ser Lys Gln His
179                    100                 105                 110
180        gcc agc cta gtg atg acc cag gac ccc tat aaa gtg agc aca ttc gag   384
181        Ala Ser Leu Val Met Thr Gln Asp Pro Tyr Lys Val Ser Thr Phe Glu
182                    115                 120                 125
183        aag cca tat gca gtg gcc atg cag tac ctg tgg cgg gac gcg ggc atc   432
184        Lys Pro Tyr Ala Val Ala Met Gln Tyr Leu Trp Arg Asp Ala Gly Ile
185                    130                 135                 140
186        cgt gca tgc tac gag cga agg cgt gaa ttc cac ctt ctg gac tcc gcg   480
187        Arg Ala Cys Tyr Glu Arg Arg Arg Glu Phe His Leu Leu Asp Ser Ala
188         145                 150                 155                 160
189        gtg tat tac ctg tca cac ctg gag cgc ata tca gag gac agc tac atc   528
190        Val Tyr Tyr Leu Ser His Leu Glu Arg Ile Ser Glu Asp Ser Tyr Ile
191                    165                 170                 175
192        ccc act gcg caa gac gtg ctg cgc agt cgc atg ccc acc aca ggc atc   576
193        Pro Thr Ala Gln Asp Val Leu Arg Ser Arg Met Pro Thr Thr Gly Ile
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194                    180                185                190
195     aat gag tac tgc ttc tcc gtg aag aaa acc aaa ctg cgc atc gtg gat      624
196     Asn Glu Tyr Cys Phe Ser Val Lys Lys Thr Lys Leu Arg Ile Val Asp
197                    195                200                205
198     gtt ggt ggc cag agg tca gag cgt agg aaa tgg att cac tgt ttc gag      672
199     Val Gly Gly Gln Arg Ser Glu Arg Arg Lys Trp Ile His Cys Phe Glu
200                    210                215                220
201     aac gtg att gcc ctc atc tac ctg gcc tcc ctg agc gag tat gac cag      720
202     Asn Val Ile Ala Leu Ile Tyr Leu Ala Ser Leu Ser Glu Tyr Asp Gln
203                225                230                235                240
204     tgc cta gag gag aac gat cag gag aac cgc atg gag gag agt ctc gct      768
205     Cys Leu Glu Glu Asn Asp Gln Glu Asn Arg Met Glu Glu Ser Leu Ala
206                            245                250                255
207     ctg ttc agc acg atc cta gag ctg ccc tgg ttc aag agc acc tcg gtc      816
208     Leu Phe Ser Thr Ile Leu Glu Leu Pro Trp Phe Lys Ser Thr Ser Val
209                        260                265                270
210     atc ctc ttc ctc aac aag acg gac atc ctg gaa gat aag att cac acc      864
211     Ile Leu Phe Leu Asn Lys Thr Asp Ile Leu Glu Asp Lys Ile His Thr
212                        275                280                285
213     tcc cac ctg gcc aca tac ttc ccc agc ttc cag gga ccc cgg cga gac      912
214     Ser His Leu Ala Thr Tyr Phe Pro Ser Phe Gln Gly Pro Arg Arg Asp
215                    290                295                300
216     gca gag gcc gcc aag agc ttc atc ttg gac atg tat gcg cgc gtg tac      960
217     Ala Glu Ala Ala Lys Ser Phe Ile Leu Asp Met Tyr Ala Arg Val Tyr
218                305                310                315                320
219     gcg agc tgc gca gag ccc cag gac ggt ggc agg aaa ggc tcc cgc gcg     1008
220     Ala Ser Cys Ala Glu Pro Gln Asp Gly Gly Arg Lys Gly Ser Arg Ala
221                            325                330                335
222     cgc cgc ttc ttc gca cac ttc acc tgt gcc acg gac acg caa agc gtc     1056
223     Arg Arg Phe Phe Ala His Phe Thr Cys Ala Thr Asp Thr Gln Ser Val
224                        340                345                350
225     cgc agc gtg ttc aag gac gtg cgg gac tcg gtg ctg gcc cgg tac ctg     1104
226     Arg Ser Val Phe Lys Asp Val Arg Asp Ser Val Leu Ala Arg Tyr Leu
227                        355                360                365
228     gac gag atc aac ctg ctg tga                                          1125
229     Asp Glu Ile Asn Leu Leu
230                    370
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233  <211> LENGTH: 374
234  <212> TYPE: PRT
235  <213> ORGANISM: Homo sapiens
236  <400> SEQUENCE: 4
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240                      20                  25                  30
241      Leu Glu Gln Lys Lys Gln Glu Arg Glu Glu Leu Lys Leu Leu Leu Leu
242                  35                  40                  45
243      Gly Pro Gly Glu Ser Gly Lys Ser Thr Phe Ile Lys Gln Met Arg Ile
```

VERIFICATION SUMMARY
PATENT APPLICATION: **US/09/468,002**

DATE: 03/31/2003
TIME: 16:26:37

Input Set : **N:\Crf3\RULE60\09468002.raw**
Output Set: **N:\CRF4\03312003\I468002.raw**